

SEQUENCE LISTING

<110> Jackson, W. James
Pace, John

<120> Chlamydia Protein, Gene Sequence and Uses Thereof

<130> 7969-086-999

<140> 09/612,402

<141> 2000-07-06

<150> 08/942,596

<151> 1997-10-02

<160> 43

<170> PatentIn version 3.0

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant Expression Vector

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Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu	
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Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr	
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Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile	
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gca gct ttg cct tta agt tgt ttt ggg aac tta tta ggg agt ttt act	651
Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr	
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Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser	
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Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu	
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Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr	
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Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu	
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Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile	
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Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr	
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Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly	
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Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile	
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Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu	
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Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly	
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Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn	
415 420 425	

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		660						665					670		
Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr	Leu
		675					680					685			
Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg	Val
	690					695					700				
Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile	Arg
705					710					715					720
Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr	Cys
				725					730					735	
Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp	Arg
			740					745					750		
Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser	Leu
		755					760					765			
Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe	Thr
	770					775					780				
Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn	His
785					790					795					800
His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Gln	Gln	Ala	Leu	Cys
				805					810					815	
Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly	Phe
			820					825					830		
Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser	Asp
		835					840					845			
Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Ala	Gly	Glu	Ile	Gly	Ala	Gly	Leu
	850					855					860				
Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn	Glu	Leu	Arg	Pro
865					870					875					880

[illegible]

<212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 12, 15
 <223> n = a, t, g, or c

 <400> 6
 gagathatgg tnccncaa 18

 <210> 7
 <211> 18
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 12, 15
 <223> n = a, t, g, or c

 <400> 7
 gagathatgg tnccncag 18

 <210> 8
 <211> 15
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 1, 7
 <223> n = a, t, g, or c

 <400> 8
 ngtytcnccr tcata 15

 <210> 9
 <211> 15
 <212> DNA
 <213> Chlamydia sp.

 <220>
 <221> modified_base
 <222> 1, 7
 <223> n = a, t, g, or c

 <400> 9
 ngtytcnccr tcgta 15

 <210> 10
 <211> 1511
 <212> DNA
 <213> Chlamydia sp.

 <400> 10
 gaaatcatgg ttcctcaagg aattttacgat ggggagacgt taactgtatc atttccctat 60
 actgttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaataa 120
 aatcttgaca attctattgc agctttgcct ttaagttggt ttgggaactt attagggagt 180
 tttactgttt tagggagagg acactcggtg actttcgaga acatacggac ttctacaaat 240
 ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300
 ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360

ggtagccaga	ctccgacgac	aacatctaca	ccgtctaata	gtactatttta	ttctaaaaca	420
gatcttttgt	tactcaataa	tgagaagttc	tcattctata	gtaatttagt	ctctggagat	480
gggggagcta	tagatgctaa	gagcttaacg	gttcaaggaa	ttagcaagct	ttgtgtcttc	540
caagaaaata	ctgctcaagc	tgatggggga	gcttgtcaag	tagtcaccag	tttctctgct	600
atggctaacg	aggctcctat	tgcccttgta	gcgaatgttg	caggagtaag	agggggaggg	660
attgctgctg	ttcaggatgg	gcagcaggga	gtgtcatcat	ctacttcaac	agaagatcca	720
gtagtaagtt	tttccagaaa	tactgcggtg	gagtttgatg	ggaacgtagc	ccgagtagga	780
ggagggattt	actcctacgg	gaacgttgct	ttcctgaata	atggaaaaac	cttgtttctc	840
aacaatgttg	cttctcctgt	ttacattgct	gctaagcaac	caacaagtgg	acaggcttct	900
aatacgagta	ataattacgg	agatggagga	gctatcttct	gtaagaatgg	tgcgcaagca	960
ggatccaata	actctggatc	agtttcttct	gatggagagg	gagtagtttt	ctttagtagc	1020
aatgtagctg	ctgggaaagg	gggagctatt	tatgccaaaa	agctctcggt	tgctaaactgt	1080
ggccctgtac	aatttttaag	gaatatcgct	aatgatgggtg	gagcgattta	tttaggagaa	1140
tctggagagc	tcagtttatc	tgctgattat	ggagatatta	ttttcgatgg	gaatcttaaa	1200
agaacagcca	aagagaatgc	tgccgatgtt	aatggcgtaa	ctgtgtcctc	acaagccatt	1260
tcgatgggat	cgggagggaa	aataacgaca	ttaagagcta	aagcagggca	tcagattctc	1320
tttaatgatc	ccatcgagat	ggcaaacgga	aataaccagc	cagcgcagtc	ttccaaactt	1380
ctaaaaatta	acgatgggtg	aggatacaca	ggggatattg	tttttgctaa	tggaagcagt	1440
actttgtacc	aaaatgttac	gatagagcaa	ggaaggattg	ttcttcgtga	aaaggcaaaa	1500
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<210> 11
 <211> 1444
 <212> DNA
 <213> Chlamydia sp.

<400> 11						
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aactccacaa	ccaccacaac	agcctcctgc	cgctaatacag	ttgatcacgc	tttccaatct	120
gcatttgtct	ctttcttctt	tgtagcaaaa	caatgcagtt	acgaatcctc	ctaccaatcc	180
tccagcgcaa	gattctcatc	ctgcagtcac	tggtagcaca	actgctgggt	ctgttacaat	240
tagtgggcct	atcttttttg	aggattttgga	tgatacacgt	tatgataggt	atgattggct	300
aggttcta	caaaaaatca	atgtcctgaa	attacagtta	gggactaagc	ccccagctaa	360
tgccccatca	gatttgactc	tagggaatga	gatgcctaag	tatggctatc	aaggaagctg	420
gaagcttgcg	tgggataccta	atacagcaaa	taatggctcct	tatactctga	aagctacatg	480
gactaaaact	gggtataatc	ctgggcctga	gcgagtagct	tctttgggtc	caaatagttt	540
atggggatcc	attttagata	tacgatctgc	gcattcagca	attcaagcaa	gtgtggatgg	600
gcgctcttat	tgctcaggat	tatgggtttc	tggagtctcg	aatttcttct	atcatgaccg	660
cgatgcttta	ggtcagggat	atcggtatat	tagtgggggt	tattccttag	gagcaaatc	720
ctactttgga	tcategatgt	ttggtctagc	atttaccgaa	gtatttggtg	gatctaaaga	780
ttatgtagt	tgctgttcca	atcatcatgc	ttgcatagga	tccgtttatc	tatctaccca	840
acaagcttta	tgtggatcct	atgtgttcgg	agatgcgttt	atccgtgcta	gctacgggtt	900
tgggaatcag	catatgaaaa	cctcatatac	atgtgcagag	gagagcgatg	ttcggtggga	960
taataactgt	ctggctggag	agattggagc	gggattaccg	attgtgatta	ctccatctaa	1020
gctctatttg	aatgagttgc	gtcctttcgt	gcaagctgag	ttttcttatg	ccgatcatga	1080
atcttttaca	gaggaaggcg	atcaagctcg	ggcattcaag	agcggacatc	tcctaaatct	1140
atcagttcct	gttgagtgga	agtttgatcg	atgttctagt	acacatccta	ataaatatag	1200
ctttatggcg	gcttatatct	gtgatgctta	tcgcaccatc	tctggtactg	agacaacgct	1260
cctatcccat	caagagacat	ggacaacaga	tgcccttcat	ttagcaagac	atggagttgt	1320
ggtagagga	tctatgtatg	cttctctaac	aagtaataata	gaagtatatg	gccatggaag	1380
atatgagtat	cgagatgctt	ctcgaggcta	tggtttgagt	gcaggaagta	gagtcgggtt	1440
ctaa						1444

<210> 12
 <211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 12						
aagggcccaa	ttacgcagag	ggtaccgaaa	ttatggttcc	tcaaggaatt	tacgat	56

<210> 13

<211> 56
 <212> DNA
 <213> Chlamydia sp.

<400> 13
 aagggcccaa ttacgcagag ggtaccctaa gaagaaggca tgccgtgcta gcggag 56

<210> 14
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 14
 aagggcccaa ttacgcagag ggtaccggag agctcgcgaa tccatacgaa taggaac 57

<210> 15
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 15
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Asn Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Pro Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Ser Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Ser Val Ser Gly Asp Gly Gly Ala Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220
 Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val Ala Asn
 225 230 235 240
 Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp Gly Gln
 245 250 255
 Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val Ser Phe
 260 265 270
 Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg Val Gly
 275 280 285
 Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn Gly Lys
 290 295 300
 Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala Ala Glu
 305 310 315 320

Gln	Pro	Thr	Asn	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asp	Asn	Tyr	Gly	Asp
				325					330					335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Ala	Gly	Ser	Asn
			340					345					350		
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		355					360					365			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
	370					375					380				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Leu	Leu	Gly	Asn	Ile	Ala	Asn
385					390					395					400
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
				405					410					415	
Ala	Asp	Tyr	Gly	Asp	Met	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala
			420					425					430		
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala
		435					440						445		
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala
	450					455						460			
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn
465					470					475					480
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu
				485					490					495	
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr
			500					505					510		
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala
		515					520						525		
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met
	530					535					540				
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln
545					550					555					560
Pro	Pro	Ala	Ala	Asn	Gln	Ser	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser
				565					570					575	
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn
			580					585					590		
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala
		595					600					605			
Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp	Leu	Asp	Asp
	610					615					620				
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp
625					630					635					640
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Pro	Ala	Asn	Ala	Pro	Ser
				645					650					655	
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser
			660					665					670		
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr
	675						680					685			
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg
	690					695					700				
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile
705					710					715					720
Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr
				725					730					735	
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe	Tyr	His	Asp
			740					745					750		
Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser
		755					760					765			
Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe
	770					775					780				
Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn
785					790					795					800
His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Lys	Gln	Ala	Leu
				805					810					815	

Cys Gly Ser Tyr Val Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 820 825 830
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 835 840 845
 Asp Val Cys Trp Asp Asn Asn Cys Leu Val Gly Glu Ile Gly Val Gly
 850 855 860
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 865 870 875 880
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 885 890 895
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Arg Ser Gly His Leu Met Asn
 900 905 910
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 915 920 925
 Pro Asn Lys Tyr Ser Phe Met Gly Ala Tyr Ile Cys Asp Ala Tyr Arg
 930 935 940
 Thr Ile Ser Gly Thr Gln Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 945 950 955 960
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Ile Val Arg Gly
 965 970 975
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 980 985 990
 Arg Tyr Glu Tyr Arg Asp Thr Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 995 1000 1005
 Ser Lys Val Arg Phe
 1010

<210> 16
 <211> 1013
 <212> PRT
 <213> Chlamydia sp.

<400> 16
 Met Gln Thr Ser Phe His Lys Phe Phe Leu Ser Met Ile Leu Ala Tyr
 1 5 10 15
 Ser Cys Cys Ser Leu Thr Gly Gly Gly Tyr Ala Ala Glu Ile Met Val
 20 25 30
 Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr
 35 40 45
 Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala Gly Glu
 50 55 60
 Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser
 65 70 75 80
 Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly His
 85 90 95
 Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu
 100 105 110
 Ser Asp Ser Ala Asn Ser Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu
 115 120 125
 Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro Ala Ala
 130 135 140
 Thr Thr Asn Asn Gly Ser Gln Thr Pro Thr Thr Ser Thr Pro Ser
 145 150 155 160
 Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn Asn Glu
 165 170 175
 Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly Thr Ile
 180 185 190
 Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys Val Phe
 195 200 205
 Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val Val Thr
 210 215 220

Ser	Phe	Ser	Ala	Met	Ala	Asn	Glu	Ala	Pro	Ile	Ala	Phe	Ile	Ala	Asn
225					230					235					240
Val	Ala	Gly	Val	Arg	Gly	Gly	Gly	Ile	Ala	Ala	Val	Gln	Asp	Gly	Gln
				245					250					255	
Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser	Thr	Glu	Asp	Pro	Val	Val	Ser	Phe
			260					265					270		
Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe	Asp	Gly	Asn	Val	Ala	Arg	Val	Gly
		275					280					285			
Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn	Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys
	290					295					300				
Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala	Ser	Pro	Val	Tyr	Ile	Ala	Ala	Glu
305					310					315					320
Gln	Pro	Thr	Asn	Gly	Gln	Ala	Ser	Asn	Thr	Ser	Asp	Asn	Tyr	Gly	Asp
				325					330					335	
Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala	Ala	Gly	Ser	Asn
			340					345					350		
Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val	Phe	Phe	Ser
		355					360					365			
Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Lys	Lys	Leu
	370					375					380				
Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Gly	Asn	Ile	Ala	Asn
385					390					395					400
Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu	Ser	Leu	Ser
				405				410						415	
Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Thr	Ala
			420					425					430		
Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser	Ser	Gln	Ala
		435					440					445			
Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg	Ala	Lys	Ala
	450					455					460				
Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala	Asn	Gly	Asn
465					470					475					480
Asn	Gln	Pro	Ala	Gln	Ser	Ser	Glu	Pro	Leu	Lys	Ile	Asn	Asp	Gly	Glu
				485				490						495	
Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Asn	Ser	Thr	Leu	Tyr
			500					505					510		
Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg	Glu	Lys	Ala
		515					520					525			
Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser	Leu	Tyr	Met
	530					535					540				
Glu	Ala	Gly	Ser	Thr	Leu	Asp	Phe	Val	Thr	Pro	Gln	Pro	Pro	Gln	Gln
545					550					555					560
Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu	His	Leu	Ser
				565				570						575	
Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro	Pro	Thr	Asn
			580					585					590		
Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser	Thr	Thr	Ala
		595					600					605			
Gly	Pro	Val	Thr	Ile	Ser	Gly	Pro	Phe	Phe	Phe	Glu	Asp	Leu	Asp	Asp
	610					615					620				
Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln	Lys	Ile	Asp
625					630					635					640
Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Gln	Pro	Ser	Ala	Asn	Ala	Pro	Ser
				645				650						655	
Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr	Gln	Gly	Ser
			660					665					670		
Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly	Pro	Tyr	Thr
		675					680					685			
Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly	Pro	Glu	Arg
	690					695					700				
Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile	Leu	Asp	Ile
705					710					715					720

Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly	Arg	Ser	Tyr
				725					730					735	
Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Ser	Tyr	His	Asp
			740					745					750		
Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly	Gly	Tyr	Ser
		755					760					765			
Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly	Leu	Ala	Phe
	770					775					780				
Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys	Arg	Ser	Asn
785					790					795					800
His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Lys	Gln	Ala	Leu
				805					810					815	
Cys	Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala	Ser	Tyr	Gly
			820					825					830		
Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala	Glu	Glu	Ser
		835					840					845			
Asp	Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Val	Gly	Glu	Ile	Gly	Val	Gly
	850					855					860				
Leu	Pro	Ile	Val	Thr	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn	Glu	Leu	Arg
865					870					875					880
Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His	Glu	Ser	Phe	Thr
				885					890					895	
Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Arg	Ser	Gly	His	Leu	Met	Asn
			900					905					910		
Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys	Ser	Ser	Thr	His
	915						920					925			
Pro	Asn	Lys	Tyr	Ser	Phe	Met	Gly	Ala	Tyr	Ile	Cys	Asp	Ala	Tyr	Arg
	930					935					940				
Thr	Ile	Ser	Gly	Thr	Gln	Thr	Thr	Leu	Leu	Ser	His	Gln	Glu	Thr	Trp
945					950					955					960
Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val	Ile	Val	Arg	Gly
				965					970					975	
Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val	Tyr	Gly	His	Gly
			980					985					990		
Arg	Tyr	Glu	Tyr	Arg	Asp	Thr	Ser	Arg	Gly	Tyr	Gly	Leu	Ser	Ala	Gly
		995					1000					1005			
Ser	Lys	Val	Arg	Phe											
	1010														

<210> 17
 <211> 505
 <212> PRT
 <213> Chlamydia sp.

<400> 17
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
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 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125

Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300
 Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala
 305 310 315 320
 Gly Ser Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val
 325 330 335
 Phe Phe Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala
 340 345 350
 Lys Lys Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn
 355 360 365
 Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys
 385 390 395 400
 Arg Thr Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser
 405 410 415
 Ser Gln Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg
 420 425 430
 Ala Lys Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala
 435 440 445
 Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn
 450 455 460
 Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser
 465 470 475 480
 Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg
 485 490 495
 Glu Lys Ala Lys Leu Ser Val Asn Ser
 500 505

<210> 18
 <211> 57
 <212> DNA
 <213> Chlamydia sp.

<400> 18
 aagggcccaa ttacgcagag ctcgagagaa attatggttc ctcaaggaat ttacgat

57

<210> 19
 <211> 20
 <212> DNA
 <213> Chlamydia sp.

<400> 19
cgctctagaa ctagtggatc 20

<210> 20
<211> 22
<212> DNA
<213> Chlamydia sp.

<400> 20
atgggttcctc aaggaattta cg 22

<210> 21
<211> 19
<212> DNA
<213> Chlamydia sp.

<400> 21
ggtcccccat cagcgggag 19

<210> 22
<211> 1515
<212> DNA
<213> Chlamydia sp.

<400> 22
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actgttatag gagatccgag tgggactact gttttttctg caggagagtt aacattaaaa 120
aatccttgaca attctattgc agctttgcct ttaagttggt ttgggaactt attagggagt 180
tttactgttt tagggagagg acactcggtg actttcgaga acatacggac ttctacaaat 240
ggggcagctc taagtaatag cgctgctgat ggactgttta ctattgaggg ttttaaagaa 300
ttatcctttt ccaattgcaa ttcattactt gccgtactgc ctgctgcaac gactaataag 360
ggtagccaga ctccgacgac aacatctaca ccgtctaata gtactattta ttctaaaaca 420
gatcttttgt tactcaataa tgagaagttc tcattctata gtaatttagt ctctggagat 480
gggggagcta tagatgctaa gagcttaacg gttcaaggaa ttagcaagct ttgtgtcttc 540
caagaaaata ctgctcaagc tgatggggga gcttggtcaag tagtcaccag tttctctgct 600
atggctaacg aggctcctat tgcctttgta gcgaatgttg caggagtaag agggggaggg 660
attgctgctg ttcaggatgg gcagcaggga gtgtcatcat ctacttcaac agaagatcca 720
gtagtaagtt tttccagaaa tactgcggtg gagtttgatg ggaacgtagc ccgagtagga 780
ggagggattt actcctacgg gaacgttgct ttcctgaata atggaaaaaac cttgtttctc 840
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agaacagcca aagagaatgc tgccgatgtt aatggcgtaa ctgtgtcctc acaagccatt 1260
tcgatgggat cgggagggaa aataacgaca ttaagagcta aagcagggca tcagattctc 1320
tttaatgata ccatcgagat ggcaaacgga aataaccagc cagcgagtc ttccaaactt 1380
ctaaaaatta acgatggtga aggatacaca ggggatattg tttttgctaa tggaagcagt 1440
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ttatcagtga attct 1515

<210> 23
<211> 3354
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 23
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ttaactgtat	cattttcccta	tactgttata	ggagatccga	gtgggactac	tgttttttct	180
gcaggagagt	taacgtttaa	aaatcttgac	aattctattg	cagcttttgc	tttaagtgtg	240
tttgggaact	tattaggag	ttttactggt	ttagggagag	gacactcggt	gactttcgag	300
aacatacgga	cttctacaaa	tggagctgca	ctaagtgaca	gcgctaatag	cgggttattt	360
actattgagg	gttttaaaga	attatctttt	tccaattgca	acccattact	tgccgtactg	420
cctgctgcaa	cgactaataa	tggtagccag	actccgtcga	caacatctac	accgttctaat	480
ggtactattt	attctaaaac	agatcttttg	ttactcaata	atgagaagtt	ctcatttctat	540
agtaattcag	tctctggaga	tgggggagct	atagatgcta	agagcttaac	ggttcaagga	600
attagcaagc	tttgtgtctt	ccaagaaaat	actgctcaag	ctgatggggg	agcttgtcaa	660
gtagtcacca	gtttctctgc	tatggctaac	gaggctccta	ttgcctttgt	agcgaatgtt	720
gcaggagtaa	gagggggagg	gattgctgct	gttcaggatg	ggcagcaggg	agtgtcatca	780
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gcagagaacg	gctcaattat	ctcagctaatt	ggcgacaatt	taacgattac	cggacaaaac	3300
catacattat	cattttacaca	ttctcaaggg	ccagttcttc	aaaattagcc	ttca	3354

<210> 24
 <211> 3324
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant Expression Vector

<400> 24

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acgttaactg	tatcatttcc	ctatactgtt	ataggagatc	cgagtgggac	tactgttttt	180
tctgcaggag	agttaacgtt	aaaaaatctt	gacaattcta	ttgcagcttt	gcctttaagt	240
tgttttggga	acttattagg	gagttttact	gttttaggga	gaggacactc	gttgactttc	300
gagaacatac	ggacttctac	aaatggagct	gcactaagtg	acagcgctaa	tagcgggtta	360
tttactattg	agggttttaa	agaattatct	ttttccaatt	gcaactcatt	acttgccgta	420
ctgcctgctg	caacgactaa	taatggtagc	cagactccga	cgacaacatc	tacaccgtct	480
aatggtacta	tttattctaa	aacagatctt	ttgttactca	ataatgagaa	gttctcattc	540
tatagtaatt	tagtctctgg	agatggggga	actatagatg	ctaagagctt	aacgggtcaa	600
ggaattagca	agctttgtgt	cttccaagaa	aatactgctc	aagctgatgg	gggagcttgt	660
caagtagtca	ccagtttctc	tgctatggct	aacgaggctc	ctattgcctt	tatagcgaat	720
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tcatctactt	caacagaa	tccagtagta	agtttttcca	gaaatactgc	ggtagagtgt	840
gatgggaacg	tagcccgagt	aggaggaggg	atttactcct	acgggaacgt	tgctttcctg	900
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caaccaacaa	atggacaggc	ttctaatacg	agtgataatt	acggagatgg	aggagctatc	1020
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ggagagggag	tagttttctt	tagtagcaat	gtagtctctg	ggaaaggggg	agctattttat	1140
gccaaaaaagc	tctcggttgc	taactgtggc	gctgtacaat	tcttagggaa	tatcgctaat	1200
gatggtggag	cgattttatt	aggagaatct	ggagagctca	gtttatctgc	tgattatgga	1260
gataattatt	tcgatgggaa	tcttaaaaga	acagccaaag	agaatgctgc	cgatgttaat	1320
ggcgtaactg	tgctctcaca	agccatttct	atgggatcgg	gagggaaaaat	aacgcacatta	1380
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aaccagccag	cgcagtcctc	cgaacctcta	aaaattaacg	atggtgaagg	atacacaggg	1500
gatattgttt	ttgctaattg	aaacagtact	ttgtaccaaa	atgttacgat	agagcaagga	1560
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<210> 25

<211> 65

<212> PRT
<213> Chlamydia sp.

<400> 25
Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
1 5 10 15
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Pro Leu
20 25 30
Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg Gly
35 40 45
His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala Ala
50 55 60

Leu
65
<210> 26
<211> 24
<212> PRT
<213> Chlamydia sp.

<400> 26
Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser
1 5 10 15
Ser Leu Leu Ala Asn Asn Ala Val
20

<210> 27
<211> 8
<212> PRT
<213> Chlamydia sp.

<400> 27
Gly Tyr Thr Gly Asp Ile Val Phe
1 5
<210> 28
<211> 7
<212> PRT
<213> Chlamydia sp.

<400> 28
Tyr Gly Asp Ile Ile Phe Asp
1 5
<210> 29
<211> 63
<212> PRT
<213> Chlamydia sp.

<400> 29
Gly Tyr Ala Ala Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu
1 5 10 15
Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly
20 25 30
Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn
35 40 45
Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly
50 55 60
<210> 30
<211> 22
<212> PRT
<213> Chlamydia sp.

<400> 30
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1 5 10 15

Ile Asn Asp Gly Glu Gly
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<210> 31
<211> 14
<212> PRT
<213> Chlamydia sp.

<400> 31
Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu
1 5 10
<210> 32
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 32
Lys Leu Ser Val Asn Ser Leu Ser Gln Thr
1 5 10
<210> 33
<211> 45
<212> PRT
<213> Chlamydia sp.

<400> 33
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu
35 40 45
<210> 34
<211> 64
<212> PRT
<213> Chlamydia sp.

<400> 34
Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly Pro Ile
1 5 10 15
Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu
20 25 30
Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly Thr Lys
35 40 45
Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu Met Pro
50 55 60
<210> 35
<211> 10
<212> PRT
<213> Chlamydia sp.

<400> 35
Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
1 5 10
<210> 36
<211> 458
<212> PRT
<213> Chlamydia sp.

<400> 36
Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu
1 5 10 15
Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly
20 25 30

Ile	Ala	Ala	Val	Gln	Asp	Gly	Gln	Gln	Gly	Val	Ser	Ser	Ser	Thr	Ser
		35					40					45			
Thr	Glu	Asp	Pro	Val	Val	Ser	Phe	Ser	Arg	Asn	Thr	Ala	Val	Glu	Phe
	50					55					60				
Asp	Gly	Asn	Val	Ala	Arg	Val	Gly	Gly	Gly	Ile	Tyr	Ser	Tyr	Gly	Asn
65					70					75				80	
Val	Ala	Phe	Leu	Asn	Asn	Gly	Lys	Thr	Leu	Phe	Leu	Asn	Asn	Val	Ala
				85					90					95	
Ser	Pro	Val	Tyr	Ile	Ala	Ala	Lys	Gln	Pro	Thr	Ser	Gly	Gln	Ala	Ser
			100					105					110		
Asn	Thr	Ser	Asn	Asn	Tyr	Gly	Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn
		115					120					125			
Gly	Ala	Gln	Ala	Gly	Ser	Asn	Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly
	130					135					140				
Glu	Gly	Val	Val	Phe	Phe	Ser	Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly
145					150					155					160
Ala	Ile	Tyr	Ala	Lys	Lys	Leu	Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln
				165					170					175	
Phe	Leu	Arg	Asn	Ile	Ala	Asn	Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu
			180					185					190		
Ser	Gly	Glu	Leu	Ser	Leu	Ser	Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp
		195					200					205			
Gly	Asn	Leu	Lys	Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly
	210					215				220					
Val	Thr	Val	Ser	Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile
225					230					235					240
Thr	Thr	Leu	Arg	Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro
				245					250					255	
Ile	Glu	Met	Ala	Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu
			260					265					270		
Leu	Lys	Ile	Asn	Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala
		275					280					285			
Asn	Gly	Ser	Ser	Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg
	290					295					300				
Ile	Val	Leu	Arg	Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln
305					310					315					320
Thr	Gly	Gly	Ser	Leu	Tyr	Met	Glu	Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val
				325					330					335	
Thr	Pro	Gln	Pro	Pro	Gln	Gln	Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr
			340					345					350		
Leu	Ser	Asn	Leu	His	Leu	Ser	Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala
		355					360					365			
Val	Thr	Asn	Pro	Pro	Thr	Asn	Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala
	370					375					380				
Val	Ile	Gly	Ser	Thr	Thr	Ala	Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile
385					390					395					400
Phe	Phe	Glu	Asp	Leu	Asp	Asp	Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu
				405					410					415	
Gly	Ser	Asn	Gln	Lys	Ile	Asn	Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys
			420					425					430		
Pro	Pro	Ala	Asn	Ala	Pro	Ser	Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro
		435					440					445			
Lys	Tyr	Gly	Tyr	Gln	Gly	Ser	Trp	Lys	Leu						
	450					455									

<210> 37
 <211> 325
 <212> PRT
 <213> Chlamydia sp.

<400> 37
 Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu Arg
 1 5 10 15

Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp Ile
 20 25 30
 Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser Tyr
 35 40 45
 Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His Asp
 50 55 60
 Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala Phe
 85 90 95
 Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser Asn
 100 105 110
 His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala Leu
 115 120 125
 Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr Gly
 130 135 140
 Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu Ser
 145 150 155 160
 Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala Gly
 165 170 175
 Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu Arg
 180 185 190
 Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe Thr
 195 200 205
 Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu Asn
 210 215 220
 Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr His
 225 230 235 240
 Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr Arg
 245 250 255
 Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr Trp
 260 265 270
 Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg Gly
 275 280 285
 Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His Gly
 290 295 300
 Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala Gly
 305 310 315 320
 Ser Arg Val Arg Phe
 325

<210> 38
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 38
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3

<210> 39
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 39
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 <210> 40
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 40
 000
 <210> 41
 <211> 0
 <212> DNA
 <213> Chlamydia sp.

<400> 41
 000
 <210> 42
 <211> 6
 <212> PRT
 <213> Chlamydia sp.

<400> 42
 Glu Ile Met Val Pro Gln
 1 5
 <210> 43
 <211> 984
 <212> PRT
 <213> Chlamydia sp.

<400> 43
 Glu Ile Met Val Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val
 1 5 10 15
 Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe
 20 25 30
 Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala
 35 40 45
 Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu
 50 55 60
 Gly Arg Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn
 65 70 75 80
 Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu
 85 90 95
 Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val
 100 105 110
 Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr
 115 120 125
 Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu
 130 135 140
 Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp
 145 150 155 160
 Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys
 165 170 175
 Leu Cys Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys
 180 185 190
 Gln Val Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala
 195 200 205
 Phe Val Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val
 210 215 220
 Gln Asp Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro
 225 230 235 240
 Val Val Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val
 245 250 255
 Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu
 260 265 270
 Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr
 275 280 285
 Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn
 290 295 300

Asn	Tyr	Gly	Asp	Gly	Gly	Ala	Ile	Phe	Cys	Lys	Asn	Gly	Ala	Gln	Ala
305					310					315					320
Gly	Ser	Asn	Asn	Ser	Gly	Ser	Val	Ser	Phe	Asp	Gly	Glu	Gly	Val	Val
				325					330					335	
Phe	Phe	Ser	Ser	Asn	Val	Ala	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala
				340				345					350		
Lys	Lys	Leu	Ser	Val	Ala	Asn	Cys	Gly	Pro	Val	Gln	Phe	Leu	Arg	Asn
		355					360					365			
Ile	Ala	Asn	Asp	Gly	Gly	Ala	Ile	Tyr	Leu	Gly	Glu	Ser	Gly	Glu	Leu
	370					375					380				
Ser	Leu	Ser	Ala	Asp	Tyr	Gly	Asp	Ile	Ile	Phe	Asp	Gly	Asn	Leu	Lys
385					390					395					400
Arg	Thr	Ala	Lys	Glu	Asn	Ala	Ala	Asp	Val	Asn	Gly	Val	Thr	Val	Ser
				405					410					415	
Ser	Gln	Ala	Ile	Ser	Met	Gly	Ser	Gly	Gly	Lys	Ile	Thr	Thr	Leu	Arg
			420					425					430		
Ala	Lys	Ala	Gly	His	Gln	Ile	Leu	Phe	Asn	Asp	Pro	Ile	Glu	Met	Ala
		435					440					445			
Asn	Gly	Asn	Asn	Gln	Pro	Ala	Gln	Ser	Ser	Lys	Leu	Leu	Lys	Ile	Asn
	450					455					460				
Asp	Gly	Glu	Gly	Tyr	Thr	Gly	Asp	Ile	Val	Phe	Ala	Asn	Gly	Ser	Ser
465					470					475					480
Thr	Leu	Tyr	Gln	Asn	Val	Thr	Ile	Glu	Gln	Gly	Arg	Ile	Val	Leu	Arg
				485				490						495	
Glu	Lys	Ala	Lys	Leu	Ser	Val	Asn	Ser	Leu	Ser	Gln	Thr	Gly	Gly	Ser
			500					505					510		
Leu	Tyr	Met	Glu	Ala	Gly	Ser	Thr	Trp	Asp	Phe	Val	Thr	Pro	Gln	Pro
		515					520					525			
Pro	Gln	Gln	Pro	Pro	Ala	Ala	Asn	Gln	Leu	Ile	Thr	Leu	Ser	Asn	Leu
	530					535					540				
His	Leu	Ser	Leu	Ser	Ser	Leu	Leu	Ala	Asn	Asn	Ala	Val	Thr	Asn	Pro
545					550					555					560
Pro	Thr	Asn	Pro	Pro	Ala	Gln	Asp	Ser	His	Pro	Ala	Val	Ile	Gly	Ser
				565					570					575	
Thr	Thr	Ala	Gly	Ser	Val	Thr	Ile	Ser	Gly	Pro	Ile	Phe	Phe	Glu	Asp
			580					585					590		
Leu	Asp	Asp	Thr	Ala	Tyr	Asp	Arg	Tyr	Asp	Trp	Leu	Gly	Ser	Asn	Gln
		595					600					605			
Lys	Ile	Asn	Val	Leu	Lys	Leu	Gln	Leu	Gly	Thr	Lys	Pro	Pro	Ala	Asn
	610					615					620				
Ala	Pro	Ser	Asp	Leu	Thr	Leu	Gly	Asn	Glu	Met	Pro	Lys	Tyr	Gly	Tyr
625					630					635					640
Gln	Gly	Ser	Trp	Lys	Leu	Ala	Trp	Asp	Pro	Asn	Thr	Ala	Asn	Asn	Gly
				645					650					655	
Pro	Tyr	Thr	Leu	Lys	Ala	Thr	Trp	Thr	Lys	Thr	Gly	Tyr	Asn	Pro	Gly
			660					665					670		
Pro	Glu	Arg	Val	Ala	Ser	Leu	Val	Pro	Asn	Ser	Leu	Trp	Gly	Ser	Ile
			675				680					685			
Leu	Asp	Ile	Arg	Ser	Ala	His	Ser	Ala	Ile	Gln	Ala	Ser	Val	Asp	Gly
	690					695					700				
Arg	Ser	Tyr	Cys	Arg	Gly	Leu	Trp	Val	Ser	Gly	Val	Ser	Asn	Phe	Phe
705					710					715					720
Tyr	His	Asp	Arg	Asp	Ala	Leu	Gly	Gln	Gly	Tyr	Arg	Tyr	Ile	Ser	Gly
				725					730					735	
Gly	Tyr	Ser	Leu	Gly	Ala	Asn	Ser	Tyr	Phe	Gly	Ser	Ser	Met	Phe	Gly
			740					745					750		
Leu	Ala	Phe	Thr	Glu	Val	Phe	Gly	Arg	Ser	Lys	Asp	Tyr	Val	Val	Cys
		755					760					765			
Arg	Ser	Asn	His	His	Ala	Cys	Ile	Gly	Ser	Val	Tyr	Leu	Ser	Thr	Gln
	770					775					780				
Gln	Ala	Leu	Cys	Gly	Ser	Tyr	Leu	Phe	Gly	Asp	Ala	Phe	Ile	Arg	Ala
785					790					795					800

Ser	Tyr	Gly	Phe	Gly	Asn	Gln	His	Met	Lys	Thr	Ser	Tyr	Thr	Phe	Ala
				805					810					815	
Glu	Glu	Ser	Asp	Val	Arg	Trp	Asp	Asn	Asn	Cys	Leu	Ala	Gly	Glu	Ile
			820					825					830		
Gly	Ala	Gly	Leu	Pro	Ile	Val	Ile	Thr	Pro	Ser	Lys	Leu	Tyr	Leu	Asn
		835					840					845			
Glu	Leu	Arg	Pro	Phe	Val	Gln	Ala	Glu	Phe	Ser	Tyr	Ala	Asp	His	Glu
	850					855					860				
Ser	Phe	Thr	Glu	Glu	Gly	Asp	Gln	Ala	Arg	Ala	Phe	Lys	Ser	Gly	His
865					870					875					880
Leu	Leu	Asn	Leu	Ser	Val	Pro	Val	Gly	Val	Lys	Phe	Asp	Arg	Cys	Ser
				885					890					895	
Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met	Ala	Ala	Tyr	Ile	Cys	Asp
			900					905					910		
Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr	Thr	Leu	Leu	Ser	His	Gln
		915					920					925			
Glu	Thr	Trp	Thr	Thr	Asp	Ala	Phe	His	Leu	Ala	Arg	His	Gly	Val	Val
	930					935					940				
Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr	Ser	Asn	Ile	Glu	Val	Tyr
945					950					955					960
Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala	Ser	Arg	Gly	Tyr	Gly	Leu
				965					970					975	
Ser	Ala	Gly	Ser	Arg	Val	Arg	Phe								
			980												